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EXAMINER	
MEHTA, ASHWIN D	

ART UNIT	PAPER NUMBER
1638	

DATE MAILED: 09/28/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/088,384	STEIMER ET AL.	
	Examiner	Art Unit	
	Ashwin Mehta	1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *11 August 2004*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-19* is/are pending in the application.

4a) Of the above claim(s) *8-12* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-7 and 13-18* is/are rejected.

7)☒ Claim(s) *19* is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☒ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *7302002*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

Election/Restrictions

1. Applicants' election without traverse of Group X, claims 1-7 and 13-19, and SEQ ID NO: 27, in the reply filed on August 11, 2004 is acknowledged. In their response, Applicants note that claims 1, 2, 4-7 and 13-16 were in Group X (response, page 5, 7th full paragraph), and label claim 3 as withdrawn in the claim amendments. However, claim 3, which recites SEQ ID NO: 27, is also in Group X, and will be examined to the extent that it reads on this elected sequence. Claims 1-7, 13-16, and new claims 17-19 have been examined in this Office action. The examined claims should be amended such that they no longer recite the non-elected sequences. Non-elected claims 8-12 have been withdrawn from consideration.

Specification

2. The disclosure is objected to because of the following informalities: The specification is missing sub-headings, except for the Examples. Different sections of the specification should be separated with sub-headings, as outlined in 37 CFR 1.77.

3. The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code, for example in the first full paragraph on page 12. Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See MPEP § 608.01.

Claim Objections

4. Claims 4, 14, and 19 are objected to for the following reasons:

In claim 4, line 2, the term --is-- should be inserted after "and".

In claim 14: in line 2, the first recitation of "length" appears to be a typographical error.

Claim 19 is objected to as being dependent upon a rejected base claim, but would be allowable if rewritten in independent form including all of the limitations of the base claim and any intervening claims.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

5. Claims 1-5 and 14-16 are rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter.

The claims are broadly drawn towards any nucleic acid having the formula RA-RB-RC, wherein RA and RC consist independently of 0-6000 nucleotides, RB consists of at least 50 nucleotides and is at least 80% identical to an aligned component sequence of SEQ ID NO: 27; or wherein RA or RC of said nucleic acid comprise one or more additional component sequences with a length of at least 50 nucleotide residues and at least 90% identity to an aligned component of SEQ ID NO: 27; or said nucleic acid comprising an open reading frame (ORF) encoding a protein comprising at least 200 amino acids being at least 85% identical to an aligned component of SEQ ID NO: 10; or said nucleic acid wherein RB consists of at least 100 nucleotides and is at

least 85% identical to an aligned component of SEQ ID NO: 27, and the nucleic acid comprises an ORF encoding a protein comprising at least 200 amino acids being at least 85% identical to an aligned component of SEQ ID NO: 10.

The claims read on a nucleic acid sequence per se which is found in nature and thus, is unpatentable to Applicants. The nucleic acid sequence, as claimed, has the same characteristics as those found naturally in the genome or as cellular precursors thereof and therefore does not constitute patentable subject matter. See *American Wood v. Fiber Disintegrating Co.*, 90 U.S. 566 (1974), *American Fruit Growers v. Brodgex Co.*, 283 U.S. 2 (1931), *Funk Brothers Seed Co. v. Kalo Inoculant Co.*, 33 U.S. 127 (1948), *Diamond v. Chakrabarty*, 206 USPQ 193 (1980). It is suggested that claim 1 be amended by replacing the article "A" with --An isolated--, to identify a product that is not found in nature.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

6. Claims 1-7 and 13-18 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

In claim 1: the recitation, "RA and RC consist independently of 0 to 6000 nucleotide residues" renders the claim indefinite. If RA and/or RC don't have any residues, then the nucleic acid will not have the formula RA-RB-RC. It is unclear if such nucleic acids are encompassed by the claim. The metes and bounds of the claim are unclear.

Further in claims 1, 2, 6, 13, 17, and 18: the recitation "RB consists of at least 50 (or 100) nucleotide residues" in claims 1 and 2 and "a nucleic acid which consists of at least 50 (or 100 or 200) nucleotide residues of a sequence that is at least 80% (or 85% or 90%) identical when aligned with a sequence" in claims 6, 13, 17, and 18 renders the claims indefinite. The recitation, "consists of" is closed language, and the recitations should therefore clearly state exactly what the RB component of claims 1 and 2 or the nucleic acid of claim 6, 13, 17, and 18 is. However, while the claims provide a minimum length for RB or the nucleic acid, they do not provide the maximum length for this component. The metes and bounds of the claims are unclear.

In claim 13: the recitation, "conveniently" renders the claim indefinite. The recitation is a relative term that has no definite meaning. What is convenient to one may not be considered convenient to another. The metes and bounds of the claim are unclear.

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

7. Claims 1-7 and 13-18 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are broadly drawn towards any nucleic acid having the formula RA-RB-RC, wherein RA and RC consist independently of 0-6000 nucleotides, RB consists of at least 50 nucleotides and is at least 80% identical to an aligned component sequence of SEQ ID NO: 27; or wherein RA or RC of said nucleic acid comprise one or more additional component sequences with a length of at least 50 nucleotide residues and at least 90% identity to an aligned component of SEQ ID NO: 27; or said nucleic acid comprising an open reading frame (ORF) encoding a protein comprising at least 200 amino acids being at least 85% identical to an aligned component of SEQ ID NO: 10; or said nucleic acid wherein RB consists of at least 100 nucleotides and is at least 85% identical to an aligned component of SEQ ID NO: 27, and the nucleic acid comprises an ORF encoding a protein comprising at least 200 amino acids being at least 85% identical to an aligned component of SEQ ID NO: 10; or a method of selecting a plant which compared to a wild type plant is impaired in transcriptional gene silencing, comprising separately preparing RNA of a series of plants, probing said RNA preparations with a nucleic acid molecule which consists of at least 50 nucleotide residues of a sequence that is at least 80% identical when aligned with a sequence from SEQ ID NO: 27, and identifying a plant whose RNA hybridizes with said nucleic acid.

The specification indicates that a comparison of transcriptional gene expression between a wild type Arabidopsis line carrying silent transgenes present in multiple copies, and a mutant Arabidopsis line, *mom1*, which is impaired in silencing of the transgene, revealed two cDNAs that were expressed in the *mom1* plant but not the wild type line (page 1). The comparison was conducted on RNA was prepared from *mom1* plants and a parental line "A", using the method of suppression subtractive hybridization. The cDNA library prepared from the RNA was screened

by inverted RNA gel blot analysis. Twelve of 500 cDNA clones initially selected showed increased abundance when hybridized with *mom1* cDNA. Comparison of total RNA from parental line A and *mom1* revealed differential expression for two of the twelve cDNA clones. The two clones were sequenced and named "TSI-A" (SEQ ID NO: 5) (TSI stands for Transciptionally Silent Information) and "TSI-B" (SEQ ID NO: 6). Both are expressed in *mom1* but not in parental line A and wild type Arabidopsis. The other clones did not show consistent differential expression (Example 1, pages 7-8). Northern blots of RNA from 2-week old *mom1* seedlings using TSI-A as the probe revealed four major transcripts of sizes 5000, 4700, 2500, and 1250 nucleotides. Hybridization using TSI-B as the probe revealed two transcripts of 5000 and 2500 nucleotides. Polyadenylated RNA, probed with either clone, only contained the 5000 and 2500 nucleotide transcripts. The specification admits that from their sizes, it is obvious that both TSI clones represent only partial cDNAs (paragraph bridging pages 9-10). Northern hybridization analysis using TSI-A as probe was conducted to examine TSI expression in other known Arabidopsis mutants in which gene silencing is affected. TSI-A expression was detected in all but one of the transcriptional silencing mutant plants tested, and in none of the post-transcriptional gene silencing mutant plants tested (page 10, 1st full paragraph). TSI-A and TSI-B were used as probes in Southern hybridizations to determine the source of their transcripts and organization. Multiple copies of TSI-A and TSI-B are present in the genome, and copy numbers were approximated to be 130-300 (paragraph bridging pages 10-11). The TSI clones are concentrated near the pericentromeric region of Arabidopsis chromosomes (page 11, 2nd full paragraph). 5' and 3' extension analysis were also conducted on the TSI-A sequence. Two clones were used for the analyses. The 5' extension yielded inserts of 2512 bp (SEQ ID NO: 1)

and 1997 bp (SEQ ID NO: 2) that were 97% identical. The 3' extensions have lengths of 1682 bp (SEQ ID NO: 3) and 1652 bp (SEQ ID NO: 4) that are 94% identical. Both 3' extensions have a 569 bp region that has 77% identity to TSI-B, suggesting that TSI-A and TSI-B are part of the same polyadenylated transcript in *mom1* (page 9, 1st full paragraph). Bases 437-2383 of SEQ ID NO: 1 encode the amino acid sequence of SEQ ID NO: 10, thought the ORF in SEQ ID NO: 1 is interrupted by a stop codon (page 3, last paragraph).

The specification also indicates that TSI-A and TSI-B were hybridized to a *mom1* cDNA library. Seven hybridizing clones contain the sequences set forth in SEQ ID NO: 7 (TSI-A-15) and 5 clones contain the sequence of SEQ ID NO: 8 (TSI-A-2), part of which is identical to SEQ ID NO: 4 (page 11, last paragraph). Sequence databases were also searched. To facilitate the search for the 5000 nucleotide transcript, the overlapping cDNAs were combined to yield a "virtual" sequence (SEQ ID NO: 9) that was used to search the Arabidopsis genomic sequence database. A BAC clone, BAC T6C20 (Accession No. AC005898), was found to have 91% identity to SEQ ID NO: 9. A chromosomal stretch, BAC F7N22 (Accession No. AF058825), was also uncovered that has 99% identity to SEQ ID NO: 7. The genomic sequence 5' to the sequence of SEQ ID NO: 7 is given in SEQ ID NO: 27 and is identical to bases 65081-68202 of BAC F7N22. The specification asserts that bases 65080 to 70370 of BAC F7N22 are 54% identical to the Athila retrotransposon, and that the TSI sequences map to the 3' part of Athila (paragraph bridging pages 12-13). TSI-A covers the part of the 3' non-coding region and TSI-B covers part of a polypurine tract and 3' LTR. The sequence of the 5' extension encodes a possible open reading frame of 648 amino acids (SEQ ID NO: 10) that has 51% identity with ORF2 of Athila. This ORF is present in BAC T6C20 and the cDNA clones (SEQ ID NOs: 1 and

2) for the 5000 and 2500 nucleotide transcripts, but is interrupted by stop codons. The ORF2 sequence in BAC F7N22 is degenerated by deletions and insertions, supporting the notion that the sequence is derived from a degenerated retrotransposon. Sequence searches for SEQ ID NO: 10 do not reveal homology to known sequences (page 13, 1st full paragraph). The transcription start site of BAC F7N22 was positioned at 65087 +/- 10 nucleotides in different mutants (page 14, 2nd full paragraph). The specification also indicates that TSI expression is not detected in wild type plants under salt or UV-C treatment or in plants inoculated with *Peronospora*. TSI transcription is detected in wild type cells grown for a long time in suspension (page 16, last paragraph).

However, the specification does not describe any nucleic acid having the formula RA-RB-RC wherein RA and RC each consist of 0-6000 bases, RB consists of at least 50 bases and is at least 80% identical to an aligned component sequence of SEQ ID NO: 27, other than the sequence of BACF7N22 (GenBank Accession No. AF058825) and sequences within the sequence listing. The specification indicates that the nucleic acids of the invention are used in a method of selecting a plant which compared to a wild type plant is impaired in transcriptional gene silencing, the method comprising probing RNA preparations of plants with the nucleic acids of the invention and identifying plants whose RNA hybridizes with said nucleic acid (paragraph bridging pages 5-6). However, the specification has not described any nucleotide sequences that differ from SEQ ID NO: 27 (the sequence elected for examination) that have the same function and which can be used as described in the specification. No biological function has been assigned to the sequence of SEQ ID NO: 27, and, as discussed above, this sequence may be derived from the 3' non-coding region of a degenerated Athila retrotransposon. The

specification does not describe the sequences of the 3' non-coding regions of other degenerated Athila retrotransposons. No information is provided at all regarding how the sequence of SEQ ID NO: 27 may be altered while retaining its ability to be used in the claimed method to hybridize to the same sequence in plants in impaired in transcriptional gene silencing. Further, SEQ ID NO: 27 consists of 1956 bases. The RB component of the claimed nucleic acids may be as small as 50 residues, only 40 (80%) of which need be identical to any aligned sequence of the 1956 bases of SEQ ID NO: 27. The specification does not teach any such nucleotide sequence, which can also have up to any 6000 nucleotide sequences in each of components RA and RC, that also has the properties of SEQ ID NO: 27. As discussed above, the specification indicates that the largest TSI transcript detected had 5000 bases. The specification does not describe a single nucleotide sequence having a size of more than 14,000 bases, as encompassed by the claims. Given the breadth of the claims and lack of guidance of the specification as discussed above, the specification fails to provide an adequate written description of the multitude of nucleic acids encompassed by the claims.

8. Claims 1-7 and 13-18 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for an isolated nucleic acid consisting of SEQ ID NO: 27 and a method of selecting a plant which compared to a wild type plant is impaired in transcriptional gene silencing, comprising probing RNA preparations of a series of plants with a nucleic acid consisting of SEQ ID NO: 27, does not reasonably provide enablement for other nucleic acids or said method comprising probing the RNA preparations with other nucleic acids. The specification does not enable any person skilled in the art to which it pertains, or with which it is

most nearly connected, to make and/or use the invention commensurate in scope with these claims.

The claims are broadly drawn towards any nucleic acid having the formula RA-RB-RC, wherein RA and RC consist independently of 0-6000 nucleotides, RB consists of at least 50 nucleotides and is at least 80% identical to an aligned component sequence of SEQ ID NO: 27; or wherein RA or RC of said nucleic acid comprise one or more additional component sequences with a length of at least 50 nucleotide residues and at least 90% identity to an aligned component of SEQ ID NO: 27; or said nucleic acid comprising an open reading frame (ORF) encoding a protein comprising at least 200 amino acids being at least 85% identical to an aligned component of SEQ ID NO: 10; or said nucleic acid wherein RB consists of at least 100 nucleotides and is at least 85% identical to an aligned component of SEQ ID NO: 27, and the nucleic acid comprises an ORF encoding a protein comprising at least 200 amino acids being at least 85% identical to an aligned component of SEQ ID NO: 10; or a method of selecting a plant which compared to a wild type plant is impaired in transcriptional gene silencing, comprising separately preparing RNA of a series of plants, probing said RNA preparations with a nucleic acid molecule which consists of at least 50 nucleotide residues of a sequence that is at least 80% identical when aligned with a sequence from SEQ ID NO: 27, and identifying a plant whose RNA hybridizes with said nucleic acid.

As discussed above, the specification indicates that 2 cDNAs, TSI-A and TSI- B (SEQ ID NOs: 5 and 6, respectively) were isolated from libraries constructed with RNA from *mom1* mutant Arabidopsis plants. The cDNAs correspond to transcripts that are expressed in the mutant plant but not in a parental line A or wild type Arabidopsis lines. TSI-A was used to

probed a *mom1* genomic cDNA library, and seven of the hybridizing clones contained the sequence set forth in SEQ ID NO: 7. A search of Arabidopsis genomic sequence databases revealed that the sequences taught in the sequence listing are found in two BAC clones, BAC T6C20 (Accession No. AC005898) and BAC F7N22 (Accession No. AF058825). A chromosomal stretch of the sequence in BAC F7N22 is 995 identical to SEQ ID NO: 7. The sequence of SEQ ID NO: 27 is 5' of SEQ ID NO: 7 and is identical to bases 65081-68202 of BAC F7N22. The specification asserts that bases 65080 to 70370 of BAC F7N22 are 54% identical to the Athila retrotransposon, and that the TSI sequences map to the 3' part of Athila. TSI-A covers the part of the 3' non-coding region and TSI-B covers part of a polypurine tract and 3' LTR. The sequence of the 5' extension encodes a possible open reading frame of 648 amino acids (SEQ ID NO: 10) that has 51% identity with ORF2 of Athila. This ORF is present in BAC T6C20 and the cDNA clones (SEQ ID NOs: 1 and 2) for the 5000 and 2500 nucleotide transcripts, but is interrupted by stop codons. The ORF2 sequence in BAC F7N22 is degenerated by deletions and insertions, supporting the notion that the sequence is derived from a degenerated retrotransposon. Sequence searches for SEQ ID NO: 10 do not reveal homology to known sequences. The transcription start site of BAC F7N22 was positioned at 65087 +/- 10 nucleotides in different mutants. The specification indicates that the nucleic acids of the invention are used in a method of selecting a plant which compared to a wild type plant is impaired in transcriptional gene silencing, the method comprising probing RNA preparations of plants with the nucleic acids of the invention and identifying plants whose RNA hybridizes with said nucleic acid.

However, the specification does not teach nucleic acids having the formula RA-RB-RC wherein RA and RC each consist of 0-6000 bases, RB consists of at least 50 bases and is at least 80% identical to an aligned component sequence of SEQ ID NO: 27, other than the sequence of BACF7N22 (GenBank Accession No. AF058825) and sequences within the sequence listing (of which SEQ ID NO: 27 is the sequence elected for examination). The specification does not teach any other nucleic acids that may be used in the same capacity as SEQ ID NO: 27. The sequence is to be used in the a method to identify plants that are impaired in transcriptional gene silencing by hybridizing to the same TSI transcript that SEQ ID NO: 27 represents. The specification does not teach how the sequence of SEQ ID NO: 27 can be changed without altering its ability to hybridize to the same TSI transcripts. These transcripts do not encode any functional products, and it is unclear how SEQ ID NO: 27 may be changed with altering its ability to hybridize to the same TSI transcripts. In the absence of further guidance, undue experimentation would be required by one skilled in the art to determine how SEQ ID NO: 27 may be altered while still retaining its ability to hybridize to expressed TSI transcripts of plants impaired in transcriptional gene silencing.

Furthermore, the claims encompass nucleic acids in which the RA and RB components can each have up to 6000 nucleotides, and can have any function. The specification does not teach the functions for any of these nucleotide sequences, other than those taught within the sequence listing. In the absence of further guidance, undue experimentation would be required by one skilled in the art to determine how to use all of the components of the claimed nucleic acids. See Genentech, Inc. v. Novo Nordisk, A/S, 42 USPQ2d 1001, 1005 (Fed. Cir. 1997), which teaches that "the specification, not the knowledge of one skilled in the art" must supply

the enabling aspects of the invention. Given the breadth of the claims, unpredictability of the art and lack of guidance of the specification as discussed above, undue experimentation would be required by one skilled in the art to make and use the claimed invention.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

9. Claims 1-5 and 14-16 are rejected under 35 U.S.C. 102(b) as being clearly anticipated by Dante, M. (GenEMBL Accession No. AF08825, 1998).

The claims are broadly drawn towards any nucleic acid having the formula RA-RB-RC, wherein RA and RC consist independently of 0-6000 nucleotides, RB consists of at least 50 nucleotides and is at least 80% identical to an aligned component sequence of SEQ ID NO: 27; or wherein RA or RC of said nucleic acid comprise one or more additional component sequences with a length of at least 50 nucleotide residues and at least 90% identity to an aligned component of SEQ ID NO: 27; or said nucleic acid comprising an open reading frame (ORF) encoding a protein comprising at least 200 amino acids being at least 85% identical to an aligned component of SEQ ID NO: 10; or said nucleic acid wherein RB consists of at least 100 nucleotides and is at least 85% identical to an aligned component of SEQ ID NO: 27, and the nucleic acid comprises

an ORF encoding a protein comprising at least 200 amino acids being at least 85% identical to an aligned component of SEQ ID NO: 10.

Dante teaches the 11,0157 base nucleotide sequence of Arabidopsis thaliana BAC clone F7N22. The nucleotide sequence contains instant SEQ ID NO: 27 at bases 65081-68202, and comprises nucleotide sequences encoding the amino acid sequence of instant SEQ ID NO: 10.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

10. Claims 1-5 and 13 are rejected under 35 U.S.C. 103(a) as being unpatentable over Dante, M. (GenEMBL Accession No. AF08825, 1998) in combination with Ausubel et al. (Short Protocols In Molecular Biology, 3rd Ed., 1997, John Wiley & Sons, Inc., New York, NY, pages 14-16 to 14-19).

The claims are broadly drawn towards any nucleic acid having the formula RA-RB-RC, wherein RA and RC consist independently of 0-6000 nucleotides, RB consists of at least 50 nucleotides and is at least 80% identical to an aligned component sequence of SEQ ID NO: 27; or wherein RA or RC of said nucleic acid comprise one or more additional component sequences with a length of at least 50 nucleotide residues and at least 90% identity to an aligned component of SEQ ID NO: 27; or said nucleic acid comprising an open reading frame (ORF) encoding a

protein comprising at least 200 amino acids being at least 85% identical to an aligned component of SEQ ID NO: 10; or said nucleic acid wherein RB consists of at least 100 nucleotides and is at least 85% identical to an aligned component of SEQ ID NO: 27, and the nucleic acid comprises an ORF encoding a protein comprising at least 200 amino acids being at least 85% identical to an aligned component of SEQ ID NO: 10; or a kit comprising said nucleic acid conveniently labeled to be used a probe.

Dante teaches a nucleic acid that has instant SEQ ID NO: 27, as discussed above.

Dante does not teach a labeled probe.

Ausubel et al. teach methods for the synthesis of ^{35}S-labelled probes.

It would have been obvious and within the scope of one of ordinary skill in the art at the time the invention was made to label the nucleic acid taught by Dante et al., for example following the method of Ausubel et al., so that it can be used a probe in hybridization reactions. One would have been motivated to do so, as nucleic acid hybridizations have been routinely conducted in the art to determine if similar nucleic acid sequences are present in other plants varieties and species.

11. Claim 19 is objected and claims 1-7 and 13-18 are rejected.

Contact Information

Any inquiry concerning this or earlier communications from the Examiner should be directed to Ashwin Mehta, whose telephone number is 571-272-0803. The Examiner can normally be reached from 8:00 A.M to 5:30 P.M. If attempts to reach the Examiner by telephone are unsuccessful, the Examiner's supervisor, Amy Nelson, can be reached at 571-272-0804. The fax phone numbers for the organization where this application or proceeding is assigned are 703-872-9306 for regular communications and 703-872-9307 for After Final communications. Patent applicants with problems or questions regarding electronic images that can be viewed in the

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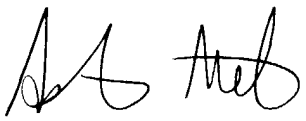

September 24, 2004

Ashwin D. Mehta, Ph.D.
Primary Examiner
Art Unit 1638